

**ANOPHELES (ANOPHELES) LESTERI BAISAS AND HU
(DIPTERA: CULICIDAE): NEOTYPE DESIGNATION AND DESCRIPTION**

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Abstract.—The Asian malaria vector, *Anopheles (Anopheles) lesteri* Baisas and Hu, 1936, is described with illustrations of the larval and pupal stages, adult female, and the male genitalia. Taxonomic and related literature records, diagnostic features, distribution, rDNA ITS2 sequence, bionomics, and medical importance of *An. lesteri* are included. A neotype female for the species from near the original type locality in Luzon, Philippines, is designated.

Key Words: *Anopheles lesteri*, Culicidae, taxonomy, description, neotype, mosquitoes, malaria

Because of the recent increase of human malaria cases in South Korea (Feighner et al. 1998, Lee et al. 1998), there is a serious need to clarify the identity of the possible mosquito vectors. Misidentifications of vector species often lead to inadequate understanding of the epidemiology of disease transmission and inadvertently affect control measures. *Anopheles (Anopheles) lesteri* Baisas and Hu, 1936, may be the most significant vector of malarial parasites in Korea, Taiwan, Japan (particularly Okinawa), and central and northern China (Harrison 1973). It is one of the 27 species of the Hyrcanus Group of *Anopheles (Anopheles)* having an Oriental or eastern Palearctic distribution (Ramsdale 2001, <http://www.mosquitocatalog.org>). It may have a potential role in malarial and filarial parasite transmission and disease outbreaks in countries where it occurs. Recently, Wilkerson et al. (2003) demonstrated that *An. anthropophagus* Xu and Feng, the most important vector malaria vector in eastern China, is actually a junior synonym of *An. lesteri*.

Anopheles lesteri was described by Baisas and Hu (1936: 214) as *An. hyrcanus* var. *lesteri* from 1 male (lot M1–8) and 1 female (lot M1–12), with corresponding larval and pupal exuviae, from Santa Mesa, Manila, Luzon, Philippines (Jose P. Ingal, coll. 2 March 1936). Many specimens (or “cotypes”) were collected from Calauan, Laguna in 1935, but type specimens were selected from the Santa Mesa specimens collected in 1936. The syntypes or type specimens (“types” and “cotypes”, collected from Santa Mesa and Calauan, Laguna, Luzon), were supposed to be deposited in the Philippine National Museum, Manila. Other specimens from the same batch were to be deposited in the National Museum of Natural History, Washington, DC, and Henry Lester Institute of Medical Research, Shanghai, China (Baisas and Hu 1936). Knight and Stone (1977: 22) noted that the type specimens could not be found. Our inquiries were also unsuccessful in search of these specimens in possible depositories in Manila and Shanghai. Specimens of *An.*

Report Documentation Page			Form Approved OMB No. 0704-0188	
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1. REPORT DATE 30 JUN 2005	2. REPORT TYPE	3. DATES COVERED 00-00-2005 to 00-00-2005		
4. TITLE AND SUBTITLE Anopheles (Anopheles) Lesteri Biases and Hu (Diptera: Culicidae): Neotype Designation and Description			5a. CONTRACT NUMBER	
			5b. GRANT NUMBER	
			5c. PROGRAM ELEMENT NUMBER	
6. AUTHOR(S)			5d. PROJECT NUMBER	
			5e. TASK NUMBER	
			5f. WORK UNIT NUMBER	
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Walter Reed Army Institute of Research, Department of Entomology, 503 Robert Grant Avenue, Silver Spring, MD, 20910-7500			8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES)			10. SPONSOR/MONITOR'S ACRONYM(S)	
			11. SPONSOR/MONITOR'S REPORT NUMBER(S)	
12. DISTRIBUTION/AVAILABILITY STATEMENT Approved for public release; distribution unlimited				
13. SUPPLEMENTARY NOTES				
14. ABSTRACT see report				
15. SUBJECT TERMS				
16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT Same as Report (SAR)	18. NUMBER OF PAGES 19
a. REPORT unclassified	b. ABSTRACT unclassified	c. THIS PAGE unclassified	19a. NAME OF RESPONSIBLE PERSON	

lesteri found in the National Museum of Natural History include 2 slides with the following labels: slide # 1—right label light yellow, with reddish border: "M 1-13 An. hyr. var. lesteri Sta. Mesa, Manila Mar. 5, 1936", left label: "Anopheles (An.) lesteri lesteri Baisas & Hu det. B.A. Harrison"; slide # 2—right label light yellow, with reddish border: "F171-50 An. lesteri cotype-male Calauan, Laguna July 15, 1935." However, larval and pupal exuviae, particularly those mounted on slide # 2, are in bad conditions (i.e., dark unknown mounting media, cracked specimens, etc.), and most morphological characters are difficult to see under the compound microscope.

Also, the original adult description (Baisas and Hu 1936) is not sufficiently complete for accurate identification of the species, and no detailed descriptions of the larval and pupal stages or of the male terminalia of specimens from the type locality (Luzon) have been made. In view of this, it becomes imperative to provide detailed descriptions of various life stages and to designate a neotype for this important species.

In the present paper, a neotype female from near the original type locality is designated for *An. lesteri* and associated ribosomal DNA internal transcribed spacer 2 (rDNA ITS2) sequence provided. Descriptions and illustrations are provided for the adult female and male, pupa and larva of this species from the same type locality.

MATERIALS AND METHODS

Except for wing spot nomenclature, which is taken from Wilkerson and Peyton (1990), for wing venation terms from Belkin (1962), and for pupal abdominal dark marks, the terminology and abbreviations of Harbach and Knight (1980, 1982) are used for the morphological characters and illustrations. Abbreviations used are as follows: E, egg; G, genitalia; L, larva; Le, larval exuviae; NE, non-existent; P, pupa; Pe, pupal exuviae; var., variety. An asterisk following the abbreviation of a given life stage indicates that at least part of the life stage

was illustrated in the publication cited. Collection codes of the most recent collections consist of a country code in capital letters followed by a collection number (e.g., PH 9-1 is an individual from collection 9 from the Philippines; a specimen number lower than 100 is used if there are associated larval and pupal exuviae, and equal or greater than 100 if there are no associated larval exuviae).

DNA isolation and sequencing. DNA was isolated by phenol-chloroform extraction, as described by Wilkerson et al. (1993), from a leg of the adult neotype female, a leg of a second female, and 2 entire males, minus genitalia, from new type locality in Calauan, Laguna. Direct sequencing was carried out as described in Wilkerson et al. (2004) using their primers. The beginning and end of the rDNA ITS2 was estimated as in Cornel et al. (1996).

TAXONOMIC TREATMENT

Anopheles (Anopheles) lesteri Baisas and Hu

(Figs. 1-4)

Anopheles yesoensis Tsuzuki 1901: 717 (*nomen dubium*).

Anopheles jesoenensis Tsuzuki 1902: 286 (*nomen dubium*).

Anopheles hyrcanus var. *lesteri* Baisas and Hu 1936: 229 (♀, P*, L*, E*). Type: Santa Mesa, Manila (Luzon), Philippines (NE), other specimens/“cotypes”: Calauan, Laguna (Luzon); Ohmori 1957: 209 (♂*, E*); Ohmori 1959: 222 (P*).

Anopheles (Anopheles) lesteri: Otsuru and Ohmori 1960: 47 (♂*, ♀*, P*, L, E*; taxonomy; bionomics; distribution, Japan: Honshu [Hyogo, Mie, Niigata, Yamaguchi], Kyushu [Kumamoto, Kagoshima, Oita, Fukuoka, Saga, Nagasaki]); Whang 1962: 39 (distribution, Korea: Tansan, Wondang, Guidandong, Yongjueup); Reid 1968: 105 (type form); Cagampang-Ramos and Darsie 1970: 14 (identification key); Basio 1971: 36 (distribution, Philippines: widely found in

Luzon including Manila, Pampanga); Basio and Reisen 1971:60 (L, distribution, Guam); Tanaka 1971: 4 (distribution, Japan: Ryukyu Islands); Harrison 1973: 4 (taxonomy); Baisas 1974: 50 (♀*, P, L*, E; taxonomy); Tanaka et al. 1979: 83 (♂* ♀*, P*, L*, E; taxonomy, bionomics, distribution, Japan: Hokkaido, Honshu, Kyushu, Ryukyu Archipelago [Amami, Okinawa Gunto, Yaeyama Gunto]); Rueda et al. 2004 (distribution, China: Hong Kong).

Anopheles (Anopheles) lesteri lesteri: Chau 1982 (distribution, China: Hong Kong).

Anopheles (Anopheles) lesteri anthropophagus Xu and Feng 1975: 81, 97 (♀*, ♂*, P*, L*, E*; taxonomy).

Anopheles (Anopheles) anthropophagus: Ma 1981: 11 (key; distribution, China: Fukien, Kiangsi, Kiangsu, Kwangsi, Kweichow, Shanghai, provinces south of Yantze River); Wilkerson et al. 2003: 1 (new synonym of *lesteri*).

Other literature records.—Otsuru 1949: 139 (as possible malaria vector, Japan); Otsuru and Ohmori 1960: 33 (bionomics, Japan); Kamimura 1968: 15 (as possible malaria vector, Japan); Reisen et al. 1972: 319 (distribution, Guam); Zhang et al. 1980: 140 (as experimental vector of Vietnam monkey malarial parasite, near *Plasmodium cynomolgi*); Xu et al. 1981: 265 (scanning electron micrographs [SEMs] of adults, pupae, eggs, China); Takai et al. 1984: 251 (hybridization, Japan); Zhang et al. 1987: 191 (vectorial capacity for malayan filariasis, Sichuan, China); Xu et al. 1988: 247 (control using insecticide-treated bed net, Guangxi, China); Ma and Wang 1988: 65 (salivary gland chromosome, China); Wang and Zheng 1989: 175 (blood meals, Guizhou, China); Ye and Zhu 1989: 256 (enzyme electrophoresis, China); Dapeng et al. 1996: 100 (as vector of *P. falciparum*, and chemical vector control, Xinyang, China); Li et al. 1991: 8 (DNA-restriction fragment length differences, China); Liu et al. 1991: 147 (as vector of malayan filariasis, Fujian,

China); Niu et al. 1992: 267 (DNA probe); Chen et al. 1994: 27–30 (trace and macro elements in hemolymph); Cheng et al. 1995: 321, (control using insecticide-treated bed net, Henan, China); Gu et al. 1966: 34 (distribution, China); Shahjehan 1996: 205 (DNA probes, China); Song and Peng 1996: 161 (control using mermithid nematodes, Sichuan, China); Xu et al. 1997: 807 (as vector of filariasis, Henan, China); Sleigh et al. 1998: 265 (as *P. vivax* vector, Henan, China); Xu et al. 1998: 135–136 (as vector of *P. vivax*; control using insecticide-treated bed net and residual spraying, Hubei, China); Kim et al. 1999: 181 (seasonal prevalence, South Korea); Zizhao et al. 1999: 240–242 (as vector of *P. falciparum* malaria, China); Lee et al. 2000: 77 (PCR, presence of *P. vivax* circumsporozoite protein, South Korea); Ma et al. 2000a: 325 (PCR assay and rDNA-ITS2 sequencing, China); Ma et al. 2000b: 36 (rDNA-ITS2, Korea); Burkett et al. 2001: 196, 2002: 45 (trap attractants, South Korea); Huang et al. 2001: 340 (habitat and distribution, Hubei, China); Coleman et al. 2002: 244 (presence of *P. vivax* circumsporozoite protein, South Korea); Min et al. 2002: 198; Shin et al. 2002: 41 (vector competence to *P. vivax*, Korea); Toma 2002: 7 (distribution review, Ryukyu Archipelago, Japan); Wilkerson et al. 2003: 1 (species molecular confirmation, rDNA-ITS2, China, Philippines, South Korea; note on geographical range, China).

ORIGINAL DESCRIPTION

In support of previous and present interpretations of the name *lesteri*, the original description given by Baisas and Hu (1936) is as follows. “Dark and pale scales of wings well contrasted. Costa—Jet black excepting for the preapical and subcostal pale spots. The subcostal spot is composed of from 10 to 22 pale scales. No scattered pale scales elsewhere on the dark portions of the costa. Subcosta—Invariably dark excepting for 1 to 4 pale scales at the apex, which form a part of the subcostal spot. Vein 1—Preapical pale spot distinct and complete.

Subcostal spot usually incomplete, seldom complete, and more rarely absent. Mid pale spot usually small and incomplete, sometimes absent. Sector pale spot usually small and incomplete. A few scattered pale scales are sometimes present on the dark area between the preapical and subcostal spots but these are not as many as those found in *nigerrimus*. A few pale scales towards the base below the presector dark spot, which do not, however, form definite spots. Vein 2—Stem mainly pale with some greyish or dark scales on lateral borders. Anterior fork dark with complete preapical pale spot. Posterior fork dark with a pale spot at about, or a little below the middle. Vein 3—A definite dark area, at base, and another at apex; apical half of intervening area with median squames mainly pale; lateral squames mainly dark; basal half mainly pale with a few scattered dark scales. Vein 4—Stem dark or mainly dark towards base below cross viens, mainly pale towards apex. Forks dark at bases and apices, the intervening portion mainly pale but lateral squames with fair distribution of dark scales. Vein 5—Apical half or more of stem pale, sometimes with a few scattered dark scales. A definite dark area a little below middle, followed by a mixture of dark and pale scales, the pale ones sometimes predominating or occupying the whole area excepting the extreme base where a few dark scales are located. Anterior fork mainly dark with the usual dark spots ill-demarcated. Sometimes the basal and sub-basal dark areas are formed on the pale portion towards the apex. Posterior fork pale excepting for the apical dark spot. Vein 6—Pale with a dark area at middle, and another one at the apex. In some specimens, a few dark scales are sometimes scattered on the pale portion towards the base. Fringe—Pale spot at apex of wing involves variable portion of area opposite vein 1 and vein 4.1. Pale spot opposite vein 5.2 absent in all males and females examined. Humeral vein—Usually with 2 or 3 dark scales. Re-

migium—Mainly dark-scaled with a few pale scales on the anterior border."

SUPPLEMENTAL DESCRIPTION FROM THIS STUDY

Female (Fig. 1).—Integument dark brown with silvery or grayish pollinosity. The following measurements and counts, $n = 6$, except when indicated. Head: Interocular space with 10–11 ($n = 3$) long, pale setae intermixed with long and small, narrow, appressed white scales; vertex, occiput and upper portion of postgena with numerous erect, truncate scales; patch of white scales on the middorsal portion of vertex; patch of dark brown to black scales on lateral portion of vertex, occiput and upper portion of postgena; long dark brown to black setae on ventral portion of postgena. Clypeus bare dorsally, with dark scales laterally. Pedicel of antenna with 6–11 ($n = 4$) small, dorsolateral, narrow to broad, grayish white spatulate scales, and 3 short, dark ventrolateral setae; flagellomere 1 with numerous narrow to broad white scales; remaining flagellomeres with a few scattered narrow to broad white scales. Scales of maxillary palpus slender, spatulate, mostly dark brown to black with intermixed dark brown setae; narrow band of white scales at base of palpomeres 3 and 4, and at base and apex of palpomere 5; apical white band of palpomere 5 slightly shorter than other basal palpomere white bands; base of maxillary palpus dorsally with single long, erect dark seta; length of maxillary palpus 1.75–1.98 mm (mean = 1.86 mm); ratio of length of each of palpomeres 2–5 to total length of palpus, 2 = 0.33–0.34 (mean = 0.34), 3 = 0.32–0.37 (mean = 0.35), 4 = 0.17–0.23 (mean = 0.20), 5 = 0.1–0.12 (mean = 0.11); ratio of combined palpomeres 2–5 to total length of palpus, 0.99–1.0 (mean = 0.99); ratio of combined palpomeres 4, 5 to total length of palpus, 0.27–0.35 (mean = 0.31); palpus 1.15–1.26 (mean = 1.22) forefemur length. Proboscis dark-scaled, except labellum light brown; base of proboscis with long, erect dark setae and scales;

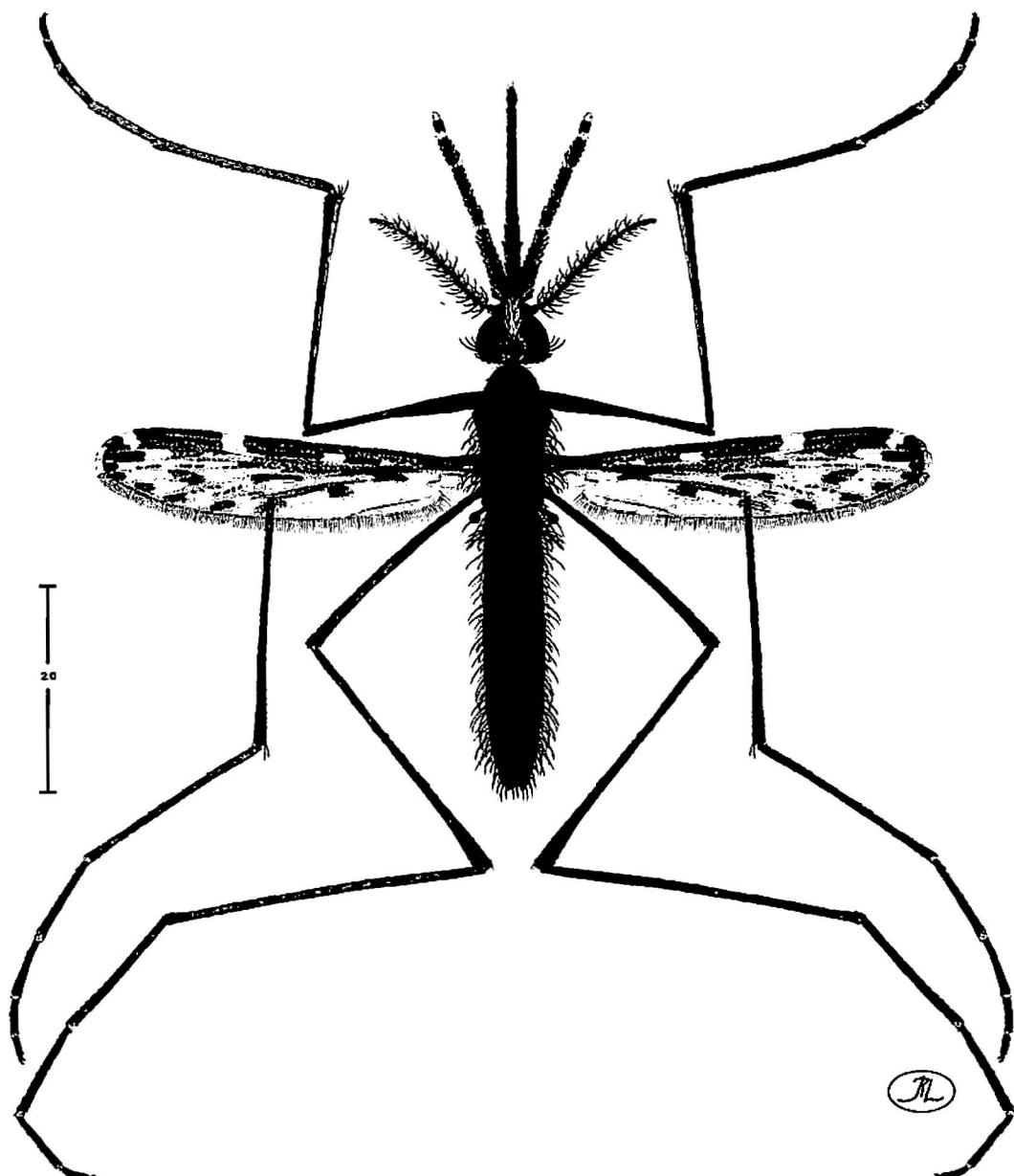


Fig. 1. *Anopheles lesteri*, adult female, habitus.

proboscis length 1.75–1.95 mm (mean = 1.86 mm, $n = 3$); proboscis 0.99–1.01 (mean = 1.0, $n = 3$) palpus length. Thorax: Scutum dark brown, with gray pollinosity; 2 submedian longitudinal lines on anterior area; a pair of indistinct black spots near antealar area; median anterior promontory with patch of intermixed narrow, short and

long pale yellow scales. Darker lateral areas of scutum with longer dark setae. Scutal fossa, antealar area and supraalar area slightly pale pollinose. Scutellum dark, slightly pale dusted, with 16–22 shorter and 14–19 long setae, short setae intermixed pale yellow and dark brown, long setae dark brown. Antepronotum with 12–14

Table 1. *Anopheles lesteri*: descriptive statistics for ratios of veins C and R-R₁, wing spot lengths/length of wing measured from humeral crossvein*.

Wing Spot	Range	Mean ± SD
Costa (C)		
Basal dark to sector dark (BD+PHD+HD+PD+SD)	0.69–0.74	0.72 ± 0.02 [0.73]
Subcostal pale (SCP)	0.03–0.07	0.05 ± 0.01 [0.05]
Preapical dark (PD)	0.27–0.31	0.29 ± 0.01 [0.29]
Preapical pale (PP)	0.03–0.05	0.04 ± 0.01 [0.03]
Apical dark (AD)	0.04–0.06	0.05 ± 0.01 [0.04]
Vein R-R₁		
Basal dark to presector dark (BD+PHD+HD+PSD)	0.38–0.41	0.40 ± 0.01 [0.38]
Sector pale (SP)	0.04–0.13	0.08 ± 0.04 [0.12]
Sector dark (SD)	0.21–0.26	0.24 ± 0.02 [0.21]
Subcostal pale (SCP)	0.05–0.06	0.05 ± 0.00 [0.06]
Preapical dark (PD)	0.24–0.29	0.26 ± 0.02 [0.25]
Preapical pale (PP)	0.04–0.06	0.05 ± 0.01 [0.06]
Apical dark (AD)	0.03–0.05	0.04 ± 0.01 [0.03]

* Six wings, from the neotype and alloneotype, and 3 individuals; [], neotype female.

dark brown setae. Pleuron brown to dark brown; upper proepisternum with 3 or 4 setae, without scales; prespiracular area with 2 or 3 setae, without scales; prealar area with 4 or 5 setae, without scales; upper mesokatepisternum with 3 or 4 setae, without scales; lower mesokatepisternum with 4 or 5 setae, without scales; upper mesepimeron with 4 or 5 setae, without scales. Legs: Fore- and midlegs dark-scaled except white scales dorsally on apex of tibia; complete narrow apical pale bands on tarsomeres 1–3, and very narrow apical dorsal pale patch on tarsomere 4; apical bands on tarsomeres 2 and 3 longest, complete ventrally, about 0.1 length of tarsomere; pale scales on tarsomere 4 dorsally and laterally only, not connected ventrally; basal pale band on tarsomere 5 absent. Hindlegs dark-scaled as fore- and midlegs, except white scales on tarsomeres 1–3 dorsally and laterally only, not ventrally. Forefemur length 1.40–1.72 mm (mean = 1.53 mm, n = 6), ratio of forefemur length to proboscis length 0.79–0.88 (mean = 0.82). Midfemur length 1.74–2.12 mm (mean = 1.94 mm), ratio of midfemur length to proboscis length 0.93–1.12 (mean = 1.04). Hindfemur length 2.01–2.2 mm (mean = 2.11 mm), ratio of

hindfemur length to proboscis length 1.07–1.21 (mean = 1.14).

Wing (Table 1): Length (measured from humeral cross vein to wing tip, excluding fringe) 2.8–3.18 mm (mean = 3.05 mm). Dark scales brown to black, pale wing scales white and pale yellow. Costa (C) dark-scaled with small subcostal pale spot (SCP, mean = 0.15) and preapical pale spot (PP, mean = 0.12); remigium dark scaled; humeral crossvein and arculus without scale patch. Subcosta (Sc) dark-scaled with few scattered spatulate white scales from base to sector dark (SD). Radius (R) to R₁ dark-scaled except 3 pale spots (SP, SCP and PP), scattered white spatulate scales from base to presector dark (PSD), and a stripe of white scales on SD before SCP; length of white stripe 0.3–0.38 mm (mean = 0.33); base of R₁ dark-scaled; bifurcation of R₂ and R₃ dark-scaled; tips of R₁, R₂, R₃ and R₄₊₅ with pale fringe. Media (M) dark-scaled with pale area before fork; bifurcation of M₁₊₂ and M₃₊₄ dark scaled; tips of M₁₊₂ and M₃₊₄ with dark fringe. Cubitus (Cu) with basal dark spot, length 0.18–0.28 (mean = 0.24); Cu₁ with 4 dark spots, length of first basal spot 0.1–0.18 mm (mean = 0.14), second spot 0.23–0.25 mm

(mean = 0.24), third spot 0.25–0.45 mm (mean = 0.33), distal fourth spot 0.13–0.3 mm (mean = 0.21); Cu_2 with distal dark spot only, length 0.18–0.25 mm (mean = 0.21); tips of Cu_1 and Cu_2 with dark fringe. Anal vein (1A) with 2 dark spots, basal spot length 0.23–0.25 mm (mean = 0.24), distal spot length 0.25–0.35 mm (mean = 0.31), tip of 1A with dark fringe. *Halter*: Scabellum, pedicel and capitellum dark brown with grayish pollinosity. *Abdomen*: Terga and sterna dark brown to black with grayish pollinosity, covered with pale brown to golden brown setae. For neotype female, descriptive statistics for ratios of costal and R-R, wing spot lengths/length of wing measured from humeral crossvein are shown in brackets in Table 1.

Male (Figs. 2C, D).—As in female except for following sexual differences. Maxillary palpus 0.94–0.98 length of proboscis (mean = 0.97; n = 4 for this and following measurements except where indicated), apex of palpomere 3 and all of palpomeres 4 and 5 enlarged. Maxillary palpus with dark brown and white scales, dorsal surface of all segments with white scales; palpomere 2 with slightly erect dark brown scales at base and light gray scales from middle to apex; palpomere 3 dark-scaled with long yellowish to light brown setae at apex; palpomere 4 pale yellow to dark brown-scaled with narrow basal white band, inner surface with long yellowish-brown to light brown setae; palpomere 5 pale brown-scaled with narrow basal white band, lateral surface with white scales and numerous dark brown short setae. Proboscis length 2.65–2.9 mm (mean = 2.69 mm), dark brown-scaled. Anal vein with single dark spot. Tergum IX (width, 2.92 mm) bare, with pair of elongate caudally directed capitate lobes; length of lobe from base to tip 0.82 distance between 2 lobes; middle of lobe narrower, 0.45 width of lobe tip and 0.42 width of lobe base. Gonocoxite 1.91–2.13× as long as wide at widest point, widest about 0.08 from base; dorsal (postrotational) surface with many long setae distally, slender fu-

siform and spatulate scales and numerous small spicules proximally; ventral surface as dorsal but with lateral scales and numerous longer spicules; mesal parabasal spine (parabasal 1) stout, borne on slightly raised base; parabasal 2 stout with slender tip; parabasal 1 base 0.07–0.15 from base of gonocoxite; parabasal 2 base 0.14–0.15 from base of gonocoxite; internal seta slender, about as long as parabasal 2, base 0.41–0.46 distance from base of gonocoxite. Gonostylus widened at base and narrowed toward middle and tip, base 2.27× wider than middle or tip; gonostylus 0.47 length of gonocoxite; gonostylus 8.89× longer than gonostylar claw. *Claspette*. Dorsal lobe of claspette with 3 closely appressed setae of about equal length; tips of 2 lateral setae curved and bluntly rounded; tip of middle seta slightly curved and round; tip of composite structure club-shaped. Ventral lobe of claspette with 2 long subapical setae, most apical much longer than other. Both ventral and dorsal lobes, and areas in between them, with numerous spicules. Aedeagal leaflets 4 per side; 2 most mesal leaflets broadest, with broad, thin, nearly transparent inner margins; other leaflets with narrow, thin, nearly transparent inner margins.

Pupa (Figs. 2A, B).—Position and development of setae as figured; range and modal number of branches, and number of branches of neotype female as in Table 2. Integument darkly pigmented. Exuviae colorless to dark brown. *Cephalothorax*: Mesothoracic wing with checkered dark stripes; metathoracic wing pigmented on middle, ventral spiracular sensilla distinct. Trumpet with dark thickened areas bearing saw-toothed or serrate edge, meatus with simple cleft, and its subbasal part with numerous spinules; trumpet length 0.30–0.45 mm (mean = 0.35 mm, n = 10 for this and following measurements and counts except where indicated), width 0.16–0.23 mm (mean = 0.13 mm, measured at base of pinna), index 1.36–2.5 (mean = 1.73); tracheoid area 0.45 length of trumpet. *Abdomen*:

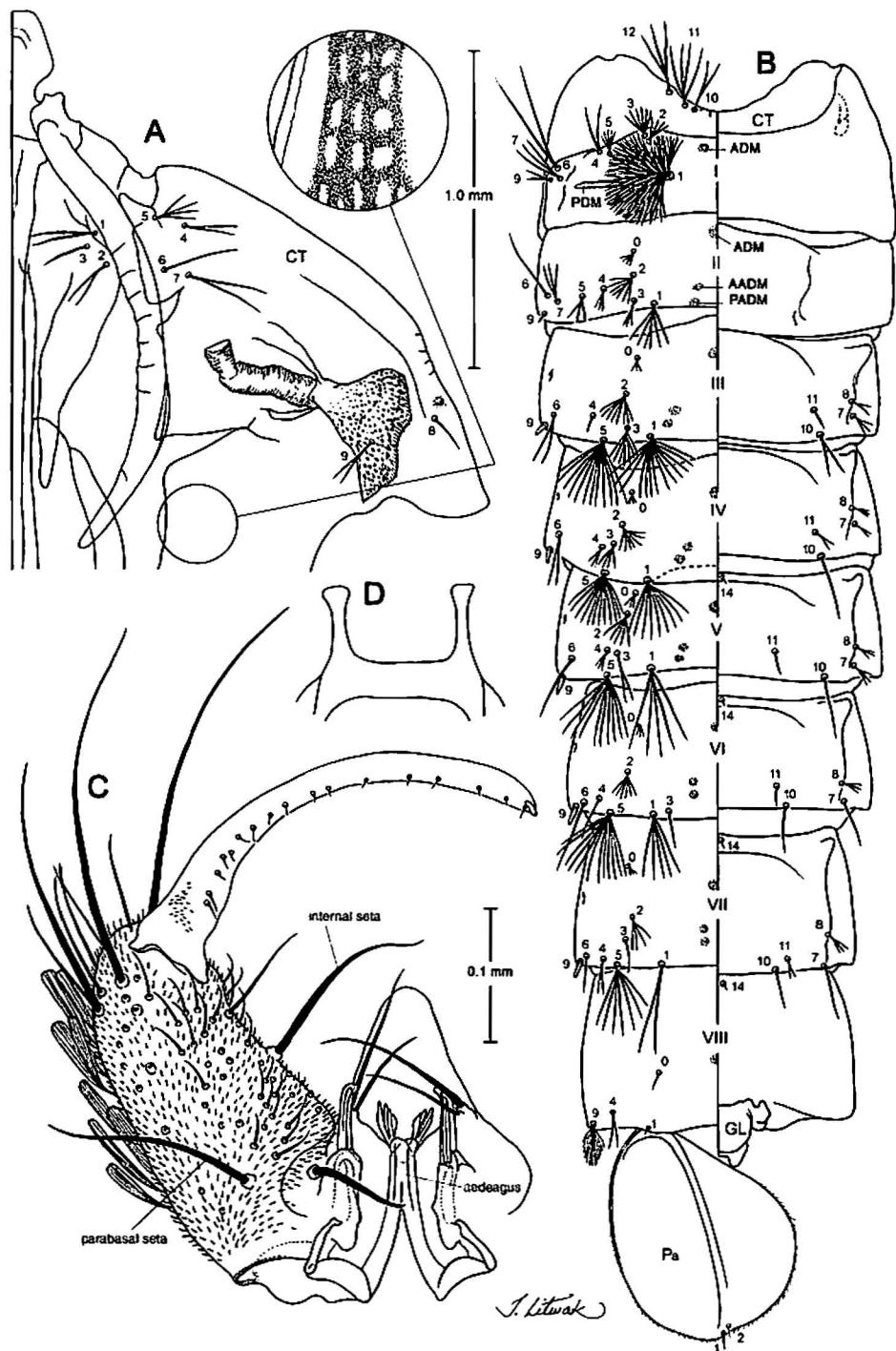


Fig. 2. *Anopheles lesteri*. (A) Pupa, cephalothorax. (B) Pupa, metathorax and abdomen, left side dorsal, right side ventral. (C) Male genitalia. (D) Tergum IX. Abbreviations used include: AADM = anterior accessory dark mark, ADM = anterior dark mark, CT = cephalothorax, GL = genital lobe, Pa = paddle, PADM = posterior accessory dark mark, PDM = posterior dark mark.

Table 2. Pupal setal branching for *Anopheles lesteri*: range (mode) based on counts made on 5–10 setae of the neotype, allonecotype, and 3 specimens collected with them; [], neotype female.

Seta No.	Cephalothorax CT	Abdominal Segments					Paddle Pa
		I	II	III	IV	V	
0	—	—	2–4(3) [4]	2–4(3) [3]	3–4(4) [4]	2–4(3) [3]	—
1	2–3(3) [2, 3]	15–23(21) [18, 16]	3–9(6) [8, 6]	13–19(13) [13, 14]	7–13(12) [12, 9]	3–6(6) [6, 3]	—
2	2–3(2) [2]	4–7(5) [4, 5]	4–10(8) [5, 7]	5–9(8) [8, 9]	3–7(5) [7]	4–7(5) [5]	—
3	1–3(1) [1, 2]	3–7(3) [6, 7]	1–3(2) [2, 3]	4–7(5) [7, 6]	3–6(5) [5, 4]	1–2(2) [2]	—
4	1–3(2) [2]	2–7(5) [5]	1–4(3) [3]	1–4(1) [1]	1–4(2) [3]	1–3(3) [3]	—
5	1–5(4) [4]	2–5(2) [2]	2–4(3) [3, 4]	10–16(13) [12, 13]	11–21(13) [12, 15]	13–24(13) [18, 19]	—
6	1–2(2) [2, 1]	1–3(2) [2]	1–2(1) [1]	1–4(2) [2]	1–2(2) [2]	1–2(1) [1, 2]	—
7	1–2(1) [1]	2–3(3) [3]	2–4(3) [3]	1–4(1) [3]	2–3(2) [3]	2–3(2) [3]	—
8	1–2(2) [2]	—	—	2–3(2) [2–3]	2–3(3) [3]	1–3(3) [3]	—
9	1–2(2) [2]	1–2(2) [2]	1 [1]	1 [1]	1 [1]	1 [1]	—
10	2 [2]	—	—	1–2(2) [2]	1–2(1) [1]	1 [1]	—
11	1–4(4) [4, 3]	—	—	1–2(1) [1]	1–2(1) [1, 2]	1–2(1) [1]	—
12	1–3(3) [3]	—	—	—	—	—	—
13	—	—	—	—	—	—	—
14	—	—	—	—	—	1 [-]	—
Seta No.	Abdominal Segments					Paddle Pa	Paddle Pa
	VI	VII	VIII	IX			
0	2–4(3) [4]	2–4(3) [2–3]	1–2(1) [1]	—	—	—	—
1	2–5(3) [4]	2–3(2) [2]	—	1 [1]	1 [1]	1 [1]	1 [1]
2	3–7(5) [7, 6]	2–4(4) [4]	—	—	—	—	—
3	1–2(1) [1, 2]	1–3(2) [1]	—	—	—	—	—
4	1–3(1) [1]	1–2(1) [1, 2]	1–2(2) [2]	—	—	—	—
5	8–17(10) [8, 10]	3–7(4) [6–7]	—	—	—	—	—
6	1–2(1) [1]	1–2(1) [1]	—	—	—	—	—
7	1–3(1) [1]	1–3(1) [1]	—	—	—	—	—
8	1–3(2) [3]	2–3(2) [2–3]	—	—	—	—	—
9	1 [1]	1 [1]	1 [1]	—	—	—	—
10	1 [1]	1–4(1) [1]	—	—	—	—	—
11	1–2(1) [1]	1–3(1) [1–2]	—	—	—	—	—
12	—	—	—	—	—	—	—
13	—	—	—	—	—	—	—
14	—	—	—	1 [1]	—	—	—

Abdominal tergum I with 2 anterior dark marks (ADM), and 2 elongate posterior dark marks (PDM); each PDM narrows mesally at base, with maximum width (0.016–0.02 mm, mean = 0.019) towards distal tip, length 0.14–0.31 mm (mean = 0.26, n = 10), about 0.12–0.28 (mean = 0.24, n = 10) width of abdominal segment I, and longer than the longest branch of seta 1-I. Abdominal terga II–VII with 1 ADM, 2 anterior accessory dark marks (AADM), and 2 posterior accessory dark marks (PADM); VIII with 1 ADM and no AADM and PADM; cuticular reticulations distinct on II–IV; spinules scattered mostly on anterior 0.37 of dorsal and lateral sides of VII and VIII. Seta 1-I fan-like with 15–23 aciculate dendritic branches; 6-I with 1–3 branches; 7-I with 2 or 3 branches; 9-I with 1 or 2 branches. Setae 1, 5-II–VII well developed; 1-V 1.04–1.31 (mean = 1.16, n = 4) length of 5-V; 1-VI 0.83–1.09 (mean = 0.97, n = 4); 1-VII 1.84–2.22 (mean = 1.09, n = 6); 3-VI aligned with and mesal of 1-VI unlike on other segments; 8-I-II absent; 9-I simple, single or forked; 9-II very short, simple, spine-like; 9-III short, with slightly rounded tip, 1.50–4.00 (mean = 2.51) length of 9-II; 9-IV strong, lightly pigmented and slightly pointed, 0.10–2.80 (mean = 1.83) length of 9-III; 9-V–VIII long, lightly pigmented and slightly pointed; 9-V 1.00–1.50 (mean = 1.68) length of 9-IV; 9-VI 0.81–1.33 (mean = 1.02) length of 9-V; 9-VII 1.00–1.34 (mean = 1.11) length of 9-VI; 9-VIII 0.80–1.06 (mean = 0.96) length of 9-VII; 9-VI 1.11–1.39 (mean = 1.27, n = 5) length of segment VI; 9-VII 1.05–1.18 (mean = 1.13, n = 5) length of segment VII; 9-VIII 0.85–0.92 (mean = 0.90, n = 5) length of segment VIII. Seta 9-I positioned near anterolateral edge of tergum; 9-II on the posterolateral edge of tergum; 9-III–VIII near posterolateral edge of tergum. Segment VII 1.05–1.19 (mean = 1.12, n = 5) length of segment VI; segment VIII 1.11–1.39 (mean = 1.26, n = 5) length of segment VI; segment VIII 1.05–1.18 (mean = 1.13, n = 5) length of

segment VII. Segment VII 0.85–0.92 (mean = 0.90, n = 5) width of segment VI (width at posterior margins); segment VIII 0.69–0.92 (mean = 0.84, n = 5) width of segment VI; segment VIII 0.75–1.01 (mean = 0.93, n = 5) width of segment VII. Width/length of segment VI 2.29–2.88 (mean = 2.48, n = 5), VII 1.84–2.21 (mean = 1.99, n = 5), VIII 1.23–1.85 (mean = 1.65, n = 5). Paddle length 0.70–0.75 mm (mean = 0.72 mm, n = 5), width 0.15–0.34 mm (mean = 0.22 mm, n = 5), length/width ratio 2.24–4.86 (mean = 3.73, n = 5); refractile index 0.34–0.67 (mean = 0.54, n = 5); paddle seta 1-Pa simple or forked (2–4 apical branches), length 0.14–0.18 mm (mean = 0.16, n = 9); 2-Pa simple or forked (2 apical branches), length 0.40–0.14 mm (mean = 0.11); length of 1-Pa 1.11–3.80 (mean = 1.66, n = 9) length of 2-Pa. Width/length of genital lobe of female 1.33–1.43 (mean = 1.37, n = 3), male 0.87–0.89 (mean = 0.88, n = 2); numerous spicules present on subapical and apical margins of genital lobe of female, absent in male.

Larva (Fig. 3).—Position and development of setae as figured; range and modal number of branches and number of branches of neotype female as shown in Table 3. **Head:** Length 0.68–0.71 mm (mean = 0.70, n = 4), width 0.66–0.76 mm (mean 0.71, n = 4). Antennal length 0.25–0.29 mm (mean = 0.26, n = 8), slightly tapered toward apex, 4.57–6.00 (mean = 5.27, n = 8) longer than wide; with spicules longer and more numerous ventrally and in vicinity of seta 1A; spicule length 0.01–0.02 mm (mean = 0.02, n = 12). Seta 1-A with 9–13 (mode = 10, n = 8) branches, length 0.16–0.24 mm (mean = 0.19, n = 8), inserted 0.11–0.22 mm (mean = 0.14, n = 8) from base of antenna; 2-A single, pointed, length 0.10–0.20 mm (mean = 0.13, n = 8); 3-A single, pointed, length 0.05–0.17 mm (mean = 0.08, n = 7); 4-A with 6–8 branches (mode = 8, n = 7); 5-A short, spine-like, 0.06–0.17 (mean = 0.13, n = 8) length of seta 1-A; 6-A spine-like about

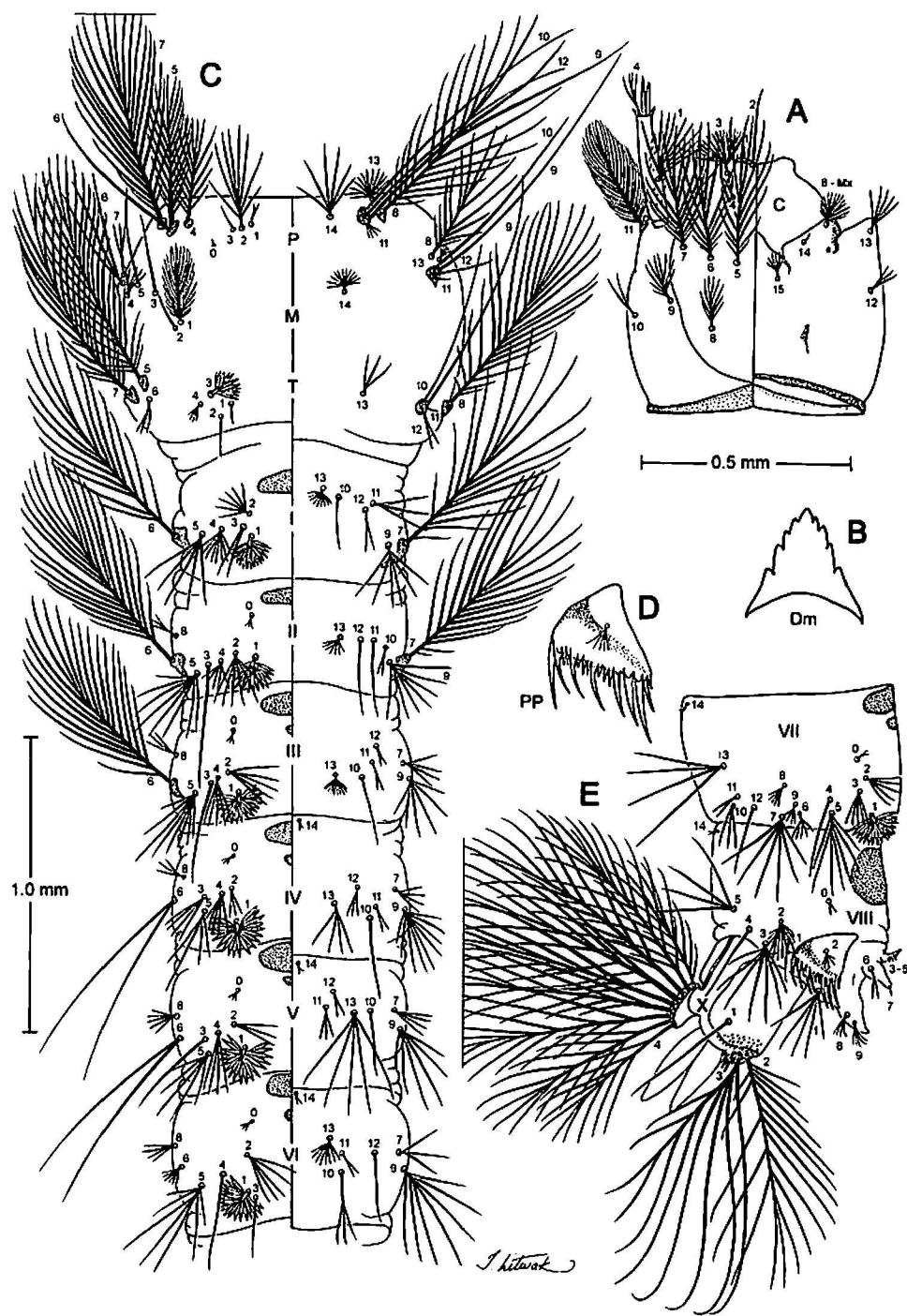


Fig. 3. *Anopheles testeri*, larva. (A) Head, left side dorsal, right side ventral. (B) Dorsumentum (Dm). (C) Thorax and abdominal segments I-VI, left side dorsal, right side ventral. (D) Pecten plate (PP) and pecten spines. (E) Abdominal segments VIII-X, side view.

Table 3. Larval setal branching for *Anopheles lesteri*: range (mode) based on counts made on 5–8 setae of the neotype and alloneotype, and 2 specimens collected with them; [], neotype female.

Seta No.	Head			Thorax			Abdominal Segments		
	C*	P	M	T	I	II	III		
0	—	—	—	—	—	—	2–4(3) [3, 4]	2–4(3) [4, 3]	
1	1 [1]	1–3(1) [2, 3]	21–29(24) [25, 27]	1 [1]	9–14(12) [13, 14]	10–15(13) [13]	18–19(19) [18, 19]		
2	1 [1]	8–12(9) [8, 9]	1–4(1) [1]	1 [1]	4–7(6) [6]	4–8(6) [6]	3–6(5) [6, 5]		
3	32–68(42) [51, 57]	1 [1]	1 [1]	9–13(11) [13, 12]	2–3(2) [2]	1 [1]	1 [1]		
4	3–5(3) [3]	12–15(15) [12]	3–5(3) [3, 5]	3–6(4) [4]	5–10(8) [8, 9]	4–8(5) [5]	3–5(5) [5, 4]		
5	11–16(15) [14, 15]	21–29(26) [26, 22]	1 [1]	25–34(29) [28, 29]	3–5(5) [5]	8–15(9) [8, 9]	5–8(7) [6, 8]		
6	11–15(15) [15]	1 [1]	3–5(3) [3, 4]	3–4(3) [3]	14–21(18) [14]	22–25(24) [24]	18–20(19) [19, 20]		
7	13–18(15) [15]	23–27(25) [27, 25]	3 [3]	22–29(25) [27]	15–20(18) [18, 16]	21–24(22) [22]	3–4(4) [4]		
8	5–13(9) [9]	15–27(22) [22, 21]	10–15(13) [10, 12]	27–30(28) [28]	—	3 [3]	3–5(3) [3]		
9	7–9(9) [7, 9]	1 [1]	1 [1]	1 [1]	6–9(6) [6, 7]	7–9(8) [7]	6–11(6) [6]		
10	1–3(2) [2]	1 [1]	1 [1]	1 [1]	1 [1]	2–3(2) [2]	1 [1]		
11	32–56(48) [56, 48]	3–4(4) [4]	1 [1]	1 [1]	3–4(3) [3, 4]	1 [1]	2 [2]		
12	2–4(3) [4, 3]	1 [1]	1 [1]	1–2(1) [1]	1–2(1) [1]	1 [1]	1–3(2) [2]		
13	3–8(3) [4, 3]	9–14(11) [11]	6–10(6) [6]	1–3(2) [2]	7–11(8) [8]	7–11(10) [7]	8–11(9) [11]		
14	1–5(5) [5]	5–9(6) [6]	8–17(10) [12, 10]	—	—	—	—		
15	6–8(8) [8, 7]	—	—	—	—	—	—		
Seta No.	Abdominal Segments								
	IV	V	VI	VII	VIII	VII	X		
0	2–4(3) [4, 3]	2–3(3) [3]	2–3(2) [3]	2–3(2) [3, 2]	1–2(1) [1]	—			
1	16–21(18) [18]	16–19(19) [19]	16–19(18) [19, 18]	14–17(17) [17]	1–2(1) [1]	1 [1]			
2	2–3(2) [2, 3]	2–3(3) [3]	3–8(5) [3, 5]	3–7(5) [4, 3]	11–12(11) [11]	16–51 (18) [19]			
3	3–4(3) [3, 4]	1 [1]	1 [1]	3–5(4) [4, 5]	7–8(7) [7, 8]	6–22(6) [12]			
4	4–6(4) [5, 4]	3–5(4) [4]	1 [1]	1 [1]	1 [1]	1 [1]	9 [9]		
5	3–5(4) [5, 4]	4–6(5) [5, 4]	6–7(6) [7]	4–8(7) [4, 5]	3–6(4) [4, 6]	—			
6	2–4(2) [2]	2 [2]	5–6(5) [6]	4–7(5) [7, 5]	1-S	4–5(4) [5]			
7	3–4(3) [3, 4]	3–4(3) [3, 4]	3–5(3) [3, 5]	3–6(6) [6]	2-S	3–5(4) [3, 4]			
8	2–3(3) [3, 2]	3–6(4) [5, 4]	3–4(4) [4]	3–5(4) [5]	6-S	2 [2]			
9	7–11(10) [10, 8]	5–9(6) [6, 5]	6–8(7) [7]	4–6(5) [6]	7-S	1 [1]			
10	1 [1]	1 [1]	2–5(3) [3, 5]	3–5(3) [3]	8-S	4–5(4) [4]			
11	2–3(2) [2]	2–5(3) [3]	2 [2]	1–2(2) [2]	9-S	3–5(5) [5]			
12	2–3(3) [3, 2]	1–4(1) [2]	1 [1]	1 [1]	—	—			
13	3–5(4) [4]	3–5(5) [5]	6–12(6) [8]	3–5(4) [4]	—	—			
14	1–2 [—]	2 [2]	2 [2]	—	1–2(1) [2]	—			
15	—	—	—	—	—	—			

* C, head; P, prothorax; M, mesothorax; T, metathorax.

1.6× longer than seta 5-A. Seta 2-C single 1.69–2.37 (mean = 1.92, $n = 3$) length of 3-C; seta 2-C close to mate of opposite side 0.002–0.006 mm (mean = 0.004, $n = 4$); 3-C densely dendritic with 32–68 main branches (mode = 42), 0.10–0.14 (mean = 0.12, $n = 8$) length of 2-C, clypeal index (distance between bases 2-C and 3-C on 1 side/distance between bases of 2-C) 11.33–40.00 (mean = 27.83, $n = 4$). *Thorax*: Seta 1-P with 1–3 branches (mode = 1, $n = 8$); 9–10,12-P single; 9–12-P setal support plate spine length 0.04 mm. Setae 9–12-M single; 9-M 3.12–12.67 (mean = 9.48, $n = 3$) length 10-M; 9–12-M setal support plate spine length 0.01–0.02 mm (mean = 0.02, $n = 4$). Setae 9–10-T single; 9-T 1.18–1.31 (mean = 1.24, $n = 4$) length of 10-T; seta 12-T with 1–3 branches; 9–12-T setal support plate spine length 0.02 mm ($n = 2$); 13-T with 3 branches. *Abdomen*. Seta 1-I with 9–14 branches (mode = 12, $n = 8$); 1-II 10–15 branches (mode = 13, $n = 8$). Seta 1-III–VII palmate with well-developed leaflets, each leaflet with short filament; 0-II–VIII and 14-III–VIII weakly developed; 0,8,14-I, 14-II absent or rare; 3-II–III,V–VI single; 3-I, IV,VII branched. Seta 1-X single, 1.30–2.40 (mean = 1.81, $n = 5$) length of saddle; 1-X inserted on saddle. Saddle with minute, sparse spicules on lateral surface. Integument of posterior margin of segment X with strongly developed dark brown to black spicules. *Spiracular apparatus*. Pecten plate with 12–18 spines; arrangement of spines alternating long and short, with 7 or 8 (mode = 7, $n = 6$) long spines and 5–11 (mode = 9, $n = 6$) short spines; long spines 1.27–11.67 (mean = 3.86, $n = 37$) length of short spines. Two posterolateral spiracular lobe plates present, each plate with elongate, slender, sclerotized projection from inner caudal margin.

Type material.—Neotype female with associated slide-mounted larval and pupal exuviae and DNA of a midleg of female; reared from a larva collected from a ditch on hill with slow flowing clear water, 28.8°C, pH 6.79, salinity 0.07 ppt, conduc-

tivity 0.15 mS, data as follows: "Tanque", Calauan, Laguna, Luzon, Philippines, L. M. Rueda Coll. 29 July 2002, 14°08'44"N, 121°18'54"E, collection and specimen no. PH 9-7. Deposited in the National Museum of Natural History, Smithsonian Institution, Washington, DC. (WRBU ACC No. 1729). Alloneotype male with slide-mounted genitalia, extracted DNA of combined head, thorax and abdomen, and associated slide-mounted pupal exuviae with collection no. PH 9-6 and same collection data as neotype female. The morphological descriptions of the head, thorax and abdomen of the alloneotype male were recorded before being processed for DNA. We were unable to collect any specimens from the original type locality of Santa Mesa, Manila, Luzon, because it is now a highly urban area totally lacking typical larval habitats. Baisas and Hu (1936) noted that many cotypes of *An. lesteri* were collected from Calauan, Laguna, Luzon, about 50 km south of Santa Mesa. This locality remains rural and we were able to collect specimens from Calauan for the present study. Morphological data in Tables 1–3 are based on measurements of the neotype, alloneotype and associated specimens collected from Calauan in 2002.

Other material examined.—247 specimens in the National Museum of Natural History, Smithsonian Institution, Washington DC, consisting of 54 ♀, 29 ♂, 76 pupal exuviae, 85 larval exuviae, and 2 ♂ genitalia. PHILIPPINES, LUZON: Province of LAGUNA, Calauan, same collection data as female neotype, PH 9-3, 1 F PeLe; PH 9-8, 1 ♀ PeLe; PH 9-11, 1 ♂ G PeLe; 17 April 1930, Lot 77-19, 1 ♂; 20 Apr. 1930, Lot 77-19, 1 ♂; 19 Jan. 1931, Lot 122, 2 ♂; 9 July 1931, Lot 247, 3 ♀; 17 Sept. 1931, 9 ♀, 3 ♂; 1 Sept. 1932, W. V. King coll., Lot K317i, 1 ♂. Province of MIN-DORO ORIENTAL, Ordovilla, 0.5 km W. Victoria, seepage spring, B. Harrison and Kol coll., 17 July 1969, P58-127, 1 Pe; B. Harrison coll., 19 July 1969, P61-37, 1 LePe; 1969, B. Harrison and Kol coll.,

1 aattagaagt ttggcaaaca gaaaactacg cagtgattgg tgctggtcac cacgtcacgg
 61 tcgtgcataa aggtgttaga gagatctcgat cgatcgctt catctcgaa ctgtgttga
 121 aaggccgcga agacagacaa gtagtaaaca gcacgcgttgc tttcccgcg atggcgaa
 181 gttctaggca ggcgcgcctt gacgctgtgt gtagatggag caggtgtctt cctcatctat
 241 ttttatttttta aaaatttgggg taagacttcc aacgtttctt cgagatagtg gaatgggctg
 301 caagagactg gaatcgaaag ttgaacaacg gaacactcta tttagcaaca ctacccagaa
 361 tccgtgcaga acgactggaa gatgcaagtt ctacctgaga atcattatca ctacagtg
 421 aggccactcg gtggtaaa

Fig. 4. Internal transcribed spacer 2 (ITS2) sequence of the ribosomal DNA for *An. lesteri* from the type locality, Calauan, Laguna, Philippines. GenBank accession number AY375469.

SEAMP Acc. 233, P44-1, 1 ♀; P58-36, 1 ♂; P58-37, 1 ♀; P58-111, 1 ♂; P58-116L, 1 ♂; P58-127, 1 ♂; Caminawit Pt., 30 Dec. 1944, G. H. Pena coll., No. C-41, 1 M. MOUNTAIN PROVINCE, Baguio, 12 June 1945, 32MSU#140, 1 ♀; S. E. Sheilds coll., 10 Aug. 1945, 24MSU#432, 12 ♀, 4 ♂; Trinidad, May 1945, J. G. Franclemont, 4 ♀, 1 ♂. Province of NUEVA ECIJA, Muñoz, Rozeboom, Knight and Laffoon coll., 8 Aug. 1945, #1153, 3 LePe. Province of PAMPANGA, Olongapo (Santa Rita), Rozeboom, Knight and Laffoon coll., 10 Aug. 1945, #1115, 4 PeLe; #1116, 1 PeLe. Province of RIZAL, Camp Nichols, PVT Carraway coll., 14 Dec. 1924, 1 ♀; 18 Dec. 1945, P469, salty fishpond with algae, 1 ♂; Mandaluyong, 17 Dec. 1945, P468, rice field, 1 ♀. VISAYAS: Province of LEYTE, Tacloban, Rozeboom, Knight and Laffoon coll., 16 Aug. 1945, No. 1713, 1 LePe, 1 ♀, 1 ♂; Southern Leyte, 2 Dec. 1944, O. H. Graham, 4 ♀, 1 ♂; Palo Alto, 1945, 1 ♀; 8 Jan. 1945, 32MSU#384a, 1 ♀; 1 Feb. 1945, 32MSU#P430, 1 ♂; 11 Mar. 1945, 32MSU#474, 1 ♀. Province of NEGROS OCCIDENTAL, La Carlota, 31 Jan. 1930, W. V. King coll., Lot 124-16, 1 ♂; Silay, 3 Feb. 1930, Lot 137, 1 ♂. Province of SAMAR, Osmena, Rozeboom, Knight and Laffoon coll., 8 Sept. 1945, #1334.30, progeny brood, 9 Le, 29 PeLe; #1334.34, 2 Le, 12 PeLe; #1348.3, 13 PeLe; #1348.6, 4 PeLe; 1945, Rozeboom, Knight, Laffoon coll., No. 1348.5, 3 M; San Antonio, 29 Nov. 1944, J. H. Paullos coll., No. 506, 1 ♀; 1 Dec. 1944, J. H. Paullos coll., No. 507, 1 ♀; Dec. 1944, 2 ♀, 3 ♂.

Molecular characterization.—DNA was extracted from a midleg of the neotype female (PH9-7), the whole body (excluding genitalia) of the alloneotype male (PH9-6), a midleg of a female (PH9-3), and the whole body (excluding genitalia) of a male (PH9-11). Ribosomal DNA ITS2 sequences are the same for all 4 (GenBank accession number AY375469 (PH9-6; Fig. 4). Other sequences in GenBank that match these sequences are as follow: under the name *An. anthropophagus*, Acc. Nos. AF384172, AJ004941, AF543860; *An. lesteri* Korea, Acc. No. AY375468); *An. lesteri* China (locally identified as *An. anthropophagus*), Acc. No. AY375467.

Distribution.—China (Hong Kong, south and central areas of the mainland, extending west to 105°E longitude and north to 43°N), Guam, Japan (including Ryukyu Islands), Korea, Philippines (Luzon: Laguna, Manila, Mindoro Oriental, Mountain Province, Nueva Ecija, Pampanga, Rizal; Visayas: Leyte, Negros Occidental, Samar).

Medical importance.—*Anopheles lesteri* is a human biter and is considered a principal vector of malaria in southern China (Beales 1984, Chow 1991, Ho et al. 1962, Ma 1981) and other areas of the country (as *anthropophagus*, Tang et al. 1991). It is suspected of being a primary vector in Japan and Korea (Kamimura 1968, Otsuru 1949, Tanaka et al. 1979). Natural infection rates of *An. lesteri* in the 1960s were 1.9 to 14.4 times greater than *An. sinensis* in China (Gu et al. 1966). In the Philippines and Guam, its biting habits are unknown, and it is not known to transmit malarial parasites.

It (as *anthropophagus*) has a strong preference for human blood, and plays an important role in the transmission of filariasis and malaria in central and south China (Xu and Feng 1975). Harrison (1973) suggested a need to determine the distribution, behavior, and malarial and filarial parasite susceptibilities of *An. lesteri* throughout its range. This species, instead of *An. sinensis*, may be the more significant vector in Taiwan, Okinawa, Japan, Korea, and central and northern China.

Bionomics.—The larvae of *An. lesteri* are found in a variety of habitats including freshwater pools, margins of ponds, lakes, areas preferably not affected by salt tides (Baisas 1974), and ditches with slowly flowing clear water in hilly areas in the Philippines. In Japan, the larvae occur in marshes, sluggish streams, ground pools, ponds, rice fields, and other impounded waters (Tanaka et al. 1979). Unlike *An. sinensis*, *An. lesteri* prefers places that are cool and shaded. Adult populations of *An. lesteri* reach their peaks during the summer season in Hokkaido (Kamimura 1976), and during June and October in Honshu and Kyushu, Japan (Otsuru and Ohmori 1960). The species is more frequently found in coastal areas than inland. In Hong Kong, it commonly occurs in hilly areas and grassy fields (Chau 1982). In Guam, *An. lesteri* larvae were found in a carabao wallow (Basio and Reisen 1971). Adults of *An. lesteri*, *An. sinensis* and other anophelines were collected in cow sheds and living rooms of houses in villages during malaria surveys in Korea (Whang 1962). *Anopheles lesteri* has been confused with *An. sinensis* and other members of the Hyrcanus Group, and some published records of its distribution and bionomics are not accurate, particularly in Japan, Korea and China.

DISCUSSION

Although Baisas and Hu (1936) provided the original description of *An. lesteri*, it was not sufficient for accurate identification of the species. This resulted in misidentifica-

tions of the species in many parts of its geographical range in Asia, particularly Korea, Japan and China. The morphological information in this paper, coupled with rDNA ITS2 sequence (Wilkerson et al. 2003), will help in solving those problems.

Anopheles lesteri has the following diagnostic features. **Adult female.** Maxillary palpus with palpomere 3 having narrow basal pale band about as wide as pale bands of other palpomeres; vein Cu₂ without apical pale fringe spot (unlike *sinensis*, *sineroides*, *pullus*); subcostal pale (SCP) spot narrow; humeral crossveins without scales (unlike *pseudosinensis*); midcoxa without upper patch of pale scales (unlike *sinensis*); hindtarsomeres 2–4 with narrow apical pale bands, hindtarsomere 4 without basal pale band (unlike *peditaeniatus*). **Adult male.** Male genitalia with dorsal lobe of claspette having 3 closely appressed setae of about equal length. Aedeagus with 4 leaflets on each side; 2 most mesal leaflets with broader transparent inner margins than other leaflets. Tergum IX bare, with pair of caudally directed elongate capitate lobes. **Pupa.** Trumpet with thick and serrate rim. Wing with checkered dark stripes. Setae 9-III–VII single, with narrowly rounded apex; seta 5-V with 13–24 branches. **Larva.** Setae 2-C, 3-P, 3, 5-M single; 3-C with 32–68 branches; 4-M with 3–5 erect branches; 9-M more than 3 times the length of 10-M; 9-M about 1.5 times longer than 10-T; 5-III with 5–8 branches; 9-III with 6–11 branches; 13-IV with 3–5 branches; 1-X strong, single about 2 times or more length of saddle; pecten with 7 or 8 long spines and 5–11 short spines. Reid (1953) and Harrison (1973) provided useful diagnostic pupal and adult morphological characters to separate *An. lesteri* from *An. sinensis*. Harrison and Scanlon (1975) also listed several characters of all life stages of 10 species of the Hyrcanus Group found in Thailand. They also discussed extensively the morphological taxonomy of the Lesteri Subgroup. Comparisons of pupal and larval characters of *An. lesteri* and related species of the Hyr-

canus Group from China and other areas of Asia are needed to further clarify species differences. Other morphological features described in this paper for larvae, pupae and adults may be helpful for separating *An. lesteri* from related species.

Morphological similarities in all stages, along with intraspecific variation of many species in the Hyrcanus Group, have lead to much confusion in Korea, Japan and China (Tanaka et al. 1979), and possibly in other areas of Asia where they occur. Wilkerson et al. (2003) suggested that the best way to infer conspecificity of populations across large geographic areas is to compare specimens from type localities. Based on the combination of published and their newly generated rDNA ITS2 sequences, Wilkerson et al. (2003) found that *An. lesteri* from South Korea and *An. anthropophagus* from Jiangsu Province, China, are the same as *An. lesteri* from near its type locality in the Philippines (Calauan, Laguna, Luzon). *Anopheles anthropophagus*, considered a major malaria vector in central and north China, is actually *An. lesteri*, not a separate species. With that finding, they placed *An. anthropophagus* in synonymy with its senior synonym, *An. lesteri*. Any morphological features previously thought to differentiate *An. anthropophagus* and *An. lesteri* are evidently variable characters of a single species. What is called *An. lesteri* in China (as reported by Gao et al. 2004: 7, 9) is actually an unknown species when compared with the work of Wilkerson et al. (2003). Several molecular studies (e.g., Li et al. 1991; Ma et al. 2000a, b; Gao et al. 2004) were conducted but were unable to clarify the taxonomic identity of *An. lesteri* found in China and Korea. With the collection of *An. lesteri* specimens from near the type locality in Luzon, Philippines, Wilkerson et al. (2003) were able to compare the specimens with those from Korea and China, and they concluded that the so called *An. anthropophagus* from China, and the so called *An. lesteri* from Korea are conspecific with *An. lesteri* from the Philippines.

With the designation of the neotype and detailed descriptions of various life stages of *An. lesteri* based on specimens collected near the type locality, future systematic studies may be conducted using various methods, including morphological, molecular or biochemical. With the identity of *An. lesteri* resolved, the effectiveness of malaria vector control practices could be further improved. As suggested by Harrison (1973), additional information is needed on the distribution, behavior, and malarial and filarial parasite susceptibilities of vector species throughout their ranges. A vector species may be a more significant parasite vector in one geographical area than in others. For example, *An. lesteri* is considered an important malaria vector in China and Korea, but not in the Philippines. Furthermore, because several species of the Hyrcanus Group are involved in the transmission of malaria and filariasis in Asia, there is a need to revise the taxonomy of the whole group and to further clarify the identities of the cryptic species, particularly the vectors, in the group.

ACKNOWLEDGMENTS

We thank Bruce A. Harrison, Yiau-Min Huang and Maria Anice M. Sallum for reviewing the manuscript and providing invaluable advice. Special thanks to the following: Taina Litwak for her illustrations; Bel Rueda, Buddy Buenavista, Lerma Buenavista, Benjie Puma, and Modesta Coronado-Puma for their help in collecting mosquitoes. Jim Pecor provided technical support in curation of specimens and preparation of slide mounts. This research was performed under a Memorandum of Understanding between the Walter Reed Army Institute of Research and the Smithsonian Institution, with institutional support provided by both organizations. The opinions and assertions contained herein are those of the authors and are not to be construed as official or reflecting the views of the Department of the Army or the Department of Defense.

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